IN THE CLAIMS:

Claims 1, 5 and 18-21 have been amended herein. All claims currently pending and under consideration in the referenced application are shown below. Applicants request that these claims be amended as indicated. This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently Amended) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of three or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each ~~said~~ alignment ~~points~~ point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

2. (Original) The method of claim 1, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

3. (Previously Presented) The method of claim 1, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

4. (Original) The method of claim 1, wherein four data traces, one for each nucleotide base type, are aligned.

5. (Currently Amended) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting a set of five or more alignment points for each data trace, said alignment points being selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers, and one or more internal peaks associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each ~~said~~ alignment ~~points~~ point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

6. (Original) The method of claim 5, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

7. (Original) The method of claim 5, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

8. (Original) The method of claim 5, wherein four data traces, one for each nucleotide base type, are aligned.

9. (Withdrawn) An apparatus for determining the positions of nucleotide bases in a target nucleic acid, comprising:

(a) a DNA sequencer comprising an electrophoresis system and a detection system for acquiring data traces reflecting the positions of nucleic acid bases in the target nucleic acid;

(b) a computer connected to the sequencer to receive the data traces, said computer comprising a processor; and

(c) a storage device operatively connected to the computer in which inner alignment points and associated reference position numbers for one or more target nucleic acids are stored,

wherein the processor is programmed to receive the data traces, access the inner alignment points and associated reference position numbers, identify peaks in the data traces and assign sequence positions numbers to the identified peaks of the data traces which maximize the number of times that the sequencing position number and the matching reference position number are assigned to a base of the same type.

10. (Previously Presented) A method for alignment of a plurality of data traces indicative of the positions of a plurality of nucleic acid base types in a target nucleic acid sequence, comprising the steps of:

(a) selecting for each data trace one or more alignment points corresponding to an internal peak associated with internal bases that are highly conserved in the target nucleic acid, and assigning to each alignment point a reference position number reflecting the relative position of the alignment point with respect to the sequence as a whole;

(b) assigning a sequence position number to each peak in each of the plurality of data traces that maximizes the number of times that the sequence position number and the reference position number are assigned to a base of the same type; and

(c) aligning the data traces based on the assigned sequence position numbers.

11. (Previously Presented) The method of claim 1, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

12. (Previously Presented) The method of claim 1, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

13. (Previously Presented) The method of claim 1, wherein four data traces, one for each nucleotide base type, are aligned.

14. (Previously Presented) The method of claim 10, further comprising alignment points selected from the group consisting of a primer peak associated with unextended primer, a full-length peak associated with full length product produced during a cyclic primer extension reaction with two primers.

15. (Previously Presented) The method of claim 14, wherein at least some of the internal peak alignment points are members of heterogeneous multiplets.

16. (Previously Presented) The method of claim 14, wherein all of the internal peak alignment points are members of heterogeneous multiplets.

17. (Previously Presented) The method of claim 14, wherein four data traces, one for each nucleotide base type, are aligned.

18. (Currently Amended) The method of claim 1, further comprising the steps of determining the average peak spacing interval between each of the alignment points and assigning sequence position numbers to peaks occurring at ~~said intervals~~ each interval, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

19. (Currently Amended) The method of claim 5, further comprising the steps of determining the average peak spacing interval between each of the alignment points and assigning a sequence position number to peaks occurring at ~~the intervals~~, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

20. (Currently Amended) The method of claim 10, further comprising the steps of determining the average peak spacing interval between each of the alignment points and assigning a sequence position number to peaks occurring at ~~the intervals~~ each interval, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.

21. (Currently Amended) The method of claim 14, further comprising the steps of determining the average peak spacing interval between each of the alignment points and assigning a sequence position number to peaks occurring at ~~the intervals~~ each interval, wherein the sequence position numbers are used for aligning the data traces based on the assigned sequence position numbers.